

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(i) APPLICANT: The Regents of the University of California

(ii) TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
PROTEIN RECEPTORS

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(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:

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- (A) ADDRESSEE: Robbins, Berliner & Carson
- (B) STREET: 201 N. Figueroa Street, 5th Floor
- (C) CITY: Los Angeles
- (D) STATE: California
- (E) COUNTRY: USA
- (F) ZIP: 90012-2628

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(v) COMPUTER READABLE FORM:

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- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

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- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

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- (A) NAME: Berliner, Robert
- (B) REGISTRATION NUMBER: 20,121
- (C) REFERENCE/DOCKET NUMBER: 5555-291

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(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 310-977-1001
- (B) TELEFAX: 310-977-1003
- (C) TELEX:

SEQUENCE LISTING

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 2232 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: cDNA

15 (iii) HYPOTHETICAL: NO

20 (iv) ANTI-SENSE: NO

25 (ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 40..1161

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

20	GGATTGAACA AGGACCCATT TCCCCAGTAC ATCCACAAAC ATG CTG TCC ACA TCT	54
	Met Leu Ser Thr Ser	
	1 5	
25	CGT TCT CGG TTT ATC AGA AAT ACC AAC GAG AGC GGT GAA GAA GTC ACC	102
	Arg Ser Arg Phe Ile Arg Asn Thr Asn Glu Ser Gly Glu Glu Val Thr	
	10 15 20	
30	ACC TTT TTT GAT TAT GAT TAC GGT GCT CCC TGT CAT AAA TTT GAC GTG	150
	Thr Phe Phe Asp Tyr Asp Tyr Gly Ala Pro Cys His Lys Phe Asp Val	
	25 30 35	
35	AAG CAA ATT GGG GCC CAA CTC CTG CCT CCG CTC TAC TCG CTG GTG TTC	198
	Lys Gln Ile Gly Ala Gln Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe	
	40 45 50	
40	ATC TTT GGT TTT GTG GGC AAC ATG CTG GTC GTC CTC ATC TTA ATA AAC	246
	Ile Phe Gly Phe Val Gly Asn Met Leu Val Val Leu Ile Leu Ile Asn	
	55 60 65	
45	TGC AAA AAG CTG AAG TGC TTG ACT GAC ATT TAC CTG CTC AAC CTG GCC	294
	Cys Lys Lys Leu Lys Cys Leu Thr Asp Ile Tyr Leu Leu Asn Leu Ala	
	70 75 80 85	
	ATC TCT GAT CTG CTT TTT CTT ATT ACT CTC CCA TTG TGG GCT CAC TCT	342
	Ile Ser Asp Leu Leu Phe Leu Ile Thr Leu Pro Leu Trp Ala His Ser	
	90 95 100	

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	GCT GCA AAT GAG TGG GTC TTT GGG AAT GCA ATG TGC AAA TTA TTC ACA	390
	Ala Ala Asn Glu Trp Val Phe Gly Asn Ala Met Cys Lys Leu Phe Thr	
	105 110 115	
5	GGG CTG TAT CAC ATC GGT TAT TTT GGC GGA ATC TTC TTC ATC ATC CTC	438
	Gly Leu Tyr His Ile Gly Tyr Phe Gly Gly Ile Phe Phe Ile Leu	
	120 125 130	
10	CTG ACA ATC GAT AGA TAC CTG GCT ATT GTC CAT GCT GTG TTT GCT TTA	486
	Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu	
	135 140 145	
15	AAA GCC AGG ACG GTC ACC TTT GGG GTG GTG ACA AGT GTG ATC ACC TGG	534
	Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr Ser Val Ile Thr Trp	
	150 155 160 165	
20	TTG GTG GCT GTG TTT GCT TCT GTC CCA GGA ATC ATC TTT ACT AAA TGC	582
	Leu Val Ala Val Phe Ala Ser Val Pro Gly Ile Ile Phe Thr Lys Cys	
	170 175 180	
25	CAG AAA GAA GAT TCT TAT GTC TGT GGC CCT TAT TTT CCA CGA GGA	630
	Gln Lys Glu Asp Ser Val Tyr Val Cys Gly Pro Tyr Phe Pro Arg Gly	
	185 190 195	
30	TGG AAT AAT TTC CAC ACA ATA ATG AGG AAC ATT TTG GGG CTG GTC CTG	678
	Trp Asn Asn Phe His Thr Ile Met Arg Asn Ile Leu Gly Leu Val Leu	
	200 205 210	
35	CCG CTG CTC ATC ATG GTC ATC TGC TAC TCG GGA ATC CTG AAA ACC CTG	726
	Pro Leu Leu Ile Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu	
	215 220 225	
40	CTT CGG TGT CGA AAC GAG AAG AAG AGG CAT AGG GCA GTG AGA GTC ATC	774
	Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Val Ile	
	230 235 240 245	
45	TTC ACC ATC ATG ATT GTT TAC TTT CTC TTC TGG ACT CCC TAT AAC ATT	822
	Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp Thr Pro Tyr Asn Ile	
	250 255 260	
	GTC ATT CTC CTG AAC ACC TTC CAG GAA TTC TTC GGC CTG AGT AAC TGT	870
	Val Ile Leu Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Ser Asn Cys	
	265 270 275	
	GAA AGC ACC AGT CAA CTG GAC CAA GCC ACG CAG GTG ACA GAG ACT CTT	918
	Glu Ser Thr Ser Gln Leu Asp Gln Ala Thr Gln Val Thr Glu Thr Leu	
	280 285 290	

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	GGG ATG ACT CAC TGC TGC ATC AAT CCC ATC ATC TAT GCC TTC GTT GGG	966	
	Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly		
295	300	305	
5	GAG AAG TTC AGA AGC CTT TTT CAC ATA GCT CTT GGC TGT AGG ATT GCC	1014	
	Glu Lys Phe Arg Ser Leu Phe His Ile Ala Leu Gly Cys Arg Ile Ala		
310	315	320	
325			
10	CCA CTC CAA AAA CCA GTG TGT GGA GGT CCA GGA GTG AGA CCA GGA AAG	1062	
	Pro Leu Gln Lys Pro Val Cys Gly Gly Pro Gly Val Arg Pro Gly Lys		
	330	335	340
15	AAT GTG AAA GTG ACT ACA CAA GGA CTC CTC GAT GGT CGT GGA AAA GGA	1110	
	Asn Val Lys Val Thr Thr Gln Gly Leu Leu Asp Gly Arg Gly Lys Gly		
	345	350	355
20	AAG TCA ATT GGC AGA GCC CCT GAA GCC AGT CTT CAG GAC AAA GAA GGA	1158	
	Lys Ser Ile Gly Arg Ala Pro Glu Ala Ser Leu Gln Asp Lys Glu Gly		
	360	365	370
25	GCC TAGAGACAGA AATGACAGAT CTCTGCTTG GAAATCACAC GTCTGGCTTC	1211	
	Ala		
30	ACAGATGTGT GATTACAGT GTGAATCTTG GTGTCTACGT TACCAAGCAG GAAGGCTGAG	1271	
	AGGAGAGAGA CTCCAGCTGG GTTGGAAAAC AGTATTTCC AAACTACCTT CCAGTTCTC	1331	
	ATTTTGAAAT ACAGGCATAG AGTCAGACT TTTTTAAAT AGTAAAAATA AAATTAAGC	1391	
	TGAAAACTGC AACTTGAAA TGTGGTAAAG AGTTAGTTG AGTTGCTATC ATGTCAAACG	1451	
	TGAAAATGCT GTATTAGTCA CAGAGATAAT TCTAGCTTG AGCTTAAGAA TTTTGAGCAG	1511	
35	GTGGTATGTT TGGGAGACTG CTGAGTCAAC CCAATAGTTG TTGATTGGCA GGAGTTGGAA	1571	
	GTGTGTGATC TGTGGGCACA TTAGCCTATG TGCATGCAGC ATCTAAGTAA TGATGTCGTT	1631	
40	TGAATCACAG TATACGCTCC ATCGCTGTCA TCTCAGCTGG ATCTCCATTC TCTCAGGCTT	1691	
	GCTGCCAAAA GCCTTTGTG TTTTGTGG TATCATTATG AAGTCATGCG TTAAATCACA	1751	
	TTCGAGTGTGTT TCAGTGCTTC GCAGATGTCC TTGATGCTCA TATTGTTCCC TAATTTGCCA	1811	
45	GTGGGAACTC CTAAATCAA TTGGCTTCTA ATCAAAGCTT TTAAACCCCTA TTGGTAAAGA	1871	
	ATGGAAGGTG GAGAAGCTCC CTGAAGTAAG CAAAGACTTT CCTCTTAGTC GAGCCAAGTT	1931	
	AAGAATGTTC TTATGTTGCC CAGTGTGTTT CTGATCTGAT GCAAGCAAGA AACACTGGC	1991	

51.

	TTCTAGAACCC AGGCAACTTG GGAACTAGAC TCCCAAGCTG GACTATGGCT CTACTTCAG	2051
	GCCACATGGC TAAAGAAGGT TTCAGAAAGA AGTGGGGACA GAGCAGAACT TTCACCTTC	2111
5	TATATTTGTA TGATCCTAAT GAATGCATAA AATGTTAAGT TGATGGTGT GAAATGTAAA	2171
	TACTGTTTTT AACAACTATG ATTTGGAAAA TAAATCAATG CTATAACTAT GTTGATAAAA	2231
10	G	2232

(2) INFORMATION FOR SEQ ID NO:2:

	(i) SEQUENCE CHARACTERISTICS:		
15	(A) LENGTH: 374 amino acids		
	(B) TYPE: amino acid		
	(D) TOPOLOGY: linear		
	(ii) MOLECULE TYPE: protein		
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:		
	Met Leu Ser Thr Ser Arg Ser Arg Phe Ile Arg Asn Thr Asn Glu Ser		
	1	5	10
25	Gly Glu Glu Val Thr Thr Phe Phe Asp Tyr Asp Tyr Gly Ala Pro Cys		
	20	25	30
	His Lys Phe Asp Val Lys Gln Ile Gly Ala Gln Leu Leu Pro Pro Leu		
30	35	40	45
	Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn Met Leu Val Val		
	50	55	60
35	Leu Ile Leu Ile Asn Cys Lys Lys Leu Lys Cys Leu Thr Asp Ile Tyr		
	65	70	75
	Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe Leu Ile Thr Leu Pro		
	85	90	95
40	Leu Trp Ala His Ser Ala Ala Asn Glu Trp Val Phe Gly Asn Ala Met		
	100	105	110
	Cys Lys Leu Phe Thr Gly Leu Tyr His Ile Gly Tyr Phe Gly Gly Ile		
45	115	120	125
	Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His		
	130	135	140

Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr
 145 150 155 160

Ser Val Ile Thr Trp Leu Val Ala Val Phe Ala Ser Val Pro Gly Ile
 5 165 170 175

Ile Phe Thr Lys Cys Gln Lys Glu Asp Ser Val Tyr Val Cys Gly Pro
 180 185 190

10 Tyr Phe Pro Arg Gly Trp Asn Asn Phe His Thr Ile Met Arg Asn Ile
 195 200 205

Leu Gly Leu Val Leu Pro Leu Leu Ile Met Val Ile Cys Tyr Ser Gly
 210 215 220

15 Ile Leu Lys Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg
 225 230 235 240

Ala Val Arg Val Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp
 20 245 250 255

Thr Pro Tyr Asn Ile Val Ile Leu Leu Asn Thr Phe Gln Glu Phe Phe
 260 265 270

25 Gly Leu Ser Asn Cys Glu Ser Thr Ser Gln Leu Asp Gln Ala Thr Gln
 275 280 285

Val Thr Glu Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile
 290 295 300

30 Tyr Ala Phe Val Gly Glu Lys Phe Arg Ser Leu Phe His Ile Ala Leu
 305 310 315 320

Gly Cys Arg Ile Ala Pro Leu Gln Lys Pro Val Cys Gly Gly Pro Gly
 35 325 330 335

Val Arg Pro Gly Lys Asn Val Lys Val Thr Thr Gln Gly Leu Leu Asp
 340 345 350

40 Gly Arg Gly Lys Gly Lys Ser Ile Gly Arg Ala Pro Glu Ala Ser Leu
 355 360 365

Gln Asp Lys Glu Gly Ala
 370

45 (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1979 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

10 (iv) ANTI-SENSE: NO

15 (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 81..1160

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

20	CAGGACTGCC TGAGACAAGC CACAAGCTGA ACAGAGAAAG TGGATTGAAC AAGGACGCAT	60
	TTCCCCAGTA CATCCACAAAC ATG CTG TCC ACA TCT CGT TCT CGG TTT ATC	110
	Met Leu Ser Thr Ser Arg Ser Arg Phe Ile	
	1 5 10	
25	AGA AAT ACC AAC GAG AGC GGT GAA GAA GTC ACC ACC TTT TTT GAT TAT	158
	Arg Asn Thr Asn Glu Ser Gly Glu Glu Val Thr Thr Phe Phe Asp Tyr	
	15 20 25	
30	GAT TAC GGT GCT CCC TGT CAT AAA TTT GAC GTG AAG CAA ATT GGG GCC	206
	Asp Tyr Gly Ala Pro Cys His Lys Phe Asp Val Lys Gln Ile Gly Ala	
	30 35 40	
35	CAA CTC CTG CCT CCG CTC TAC TCG CTG GTG TTC ATC TTT GGT TTT GTG	254
	Gln Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val	
	45 50 55	
40	GGC AAC ATG CTG GTC CTC ATC TTA ATA AAC TGC AAA AAG CTG AAG	302
	Gly Asn Met Leu Val Val Leu Ile Leu Ile Asn Cys Lys Leu Lys	
	60 65 70	
45	TGC TTG ACT GAC ATT TAC CTG CTC AAC CTG GCC ATC TCT GAT CTG CTT	350
	Cys Leu Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu	
	75 80 85 90	
	TTT CTT ATT ACT CTC CCA TTG TGG GCT CAC TCT GCT GCA AAT GAG TGG	398
	Phe Leu Ile Thr Leu Pro Leu Trp Ala His Ser Ala Ala Asn Glu Trp	
	95 100 105	

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	GTC TTT GGG AAT GCA ATG TGC AAA TTA TTC ACA GGG CTG TAT CAC ATC	446
	Val Phe Gly Asn Ala Met Cys Lys Leu Phe Thr Gly Leu Tyr His Ile	
	110 115 120	
5	GGT TAT TTT GGC GGA ATC TTC TTC ATC ATC CTC CTG ACA ATC GAT AGA	494
	Gly Tyr Phe Gly Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg	
	125 130 135	
10	TAC CTG GCT ATT GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG GTC	542
	Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val	
	140 145 150	
15	ACC TTT GGG GTG GTG ACA AGT GTG ATC ACC TGG TTG GTG GCT GTG TTT	590
	Thr Phe Gly Val Val Thr Ser Val Ile Thr Trp Leu Val Ala Val Phe	
	155 160 165 170	
	GCT TCT GTC CCA GGA ATC ATC TTT ACT AAA TGC CAG AAA GAA GAT TCT	638
	Ala Ser Val Pro Gly Ile Ile Phe Thr Lys Cys Gln Lys Glu Asp Ser	
	175 180 185	
20	GTT TAT GTC TGT GGC CCT TAT TTT CCA CGA GGA TGG AAT AAT TTC CAC	686
	Val Tyr Val Cys Gly Pro Tyr Phe Pro Arg Gly Trp Asn Asn Phe His	
	190 195 200	
25	ACA ATA ATG AGG AAC ATT TTG GGG CTG GTC CTG CCG CTG CTC ATC ATG	734
	Thr Ile Met Arg Asn Ile Leu Gly Leu Val Leu Pro Leu Leu Ile Met	
	205 210 215	
30	GTC ATC TGC TAC TCG GGA ATC CTG AAA ACC CTG CTT CGG TGT CGA AAC	782
	Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys Arg Asn	
	220 225 230	
35	GAG AAG AAG AGG CAT AGG GCA GTG AGA GTC ATC TTC ACC ATC ATG ATT	830
	Glu Lys Lys Arg His Arg Ala Val Arg Val Ile Phe Thr Ile Met Ile	
	235 240 245 250	
	GTT TAC TTT CTC TTC TGG ACT CCC TAT AAC ATT GTC ATT CTC CTG AAC	878
	Val Tyr Phe Leu Phe Trp Thr Pro Tyr Asn Ile Val Ile Leu Leu Asn	
	255 260 265	
40	ACC TTC CAG GAA TTC TTC GGC CTG AGT AAC TGT GAA AGC ACC AGT CAA	926
	Thr Phe Gln Glu Phe Phe Gly Leu Ser Asn Cys Glu Ser Thr Ser Gln	
	270 275 280	
45	CTG GAC CAA GCC ACG CAG GTG ACA GAG ACT CTT GGG ATG ACT CAC TGC	974
	Leu Asp Gln Ala Thr Gln Val Thr Glu Thr Leu Gly Met Thr His Cys	
	285 290 295	

	TGC ATC AAT CCC ATC ATC TAT GCC TTC GTT GGG GAG AAG TTC AGA AGG	1022
	Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe Arg Arg	
	300	305
		310
5	TAT CTC TCG GTG TTC TTC CGA AAG CAC ATC ACC AAG CGC TTC TGC AAA	1070
	Tyr Leu Ser Val Phe Phe Arg Lys His Ile Thr Lys Arg Phe Cys Lys	
	315	320
		325
		330
10	CAA TGT CCA GTT TTC TAC AGG GAG ACA GTG GAT GGA GTG ACT TCA ACA	1118
	Gln Cys Pro Val Phe Tyr Arg Glu Thr Val Asp Gly Val Thr Ser Thr	
	335	340
		345
15	AAC ACG CCT TCC ACT GGG GAG CAG GAA GTC TCG GCT GGT TTA	1160
	Asn Thr Pro Ser Thr Gly Glu Gln Glu Val Ser Ala Gly Leu	
	350	355
		360
	TAAAACGAGG AGCAGTTGA TTGTTGTTA TAAAGGGAGA TAACAATCTG TATATAACAA	1220
20	CAAACCTCAA GGGTTGTTG ACAATAGAA ACCTGTAAAG CAGGTGCCA GGAACCTCAG	1280
	GGCTGTGTGT ACTAATACAG ACTATGTCAC CCAATGCATA TCCAACATGT GCTCAGGGAA	1340
	TAATCCAGAA AAACGTGGG TAGAGACTTT GACTCTCCAG AAAGCTCATC TCAGCTCCTG	1400
25	AAAAATGCCT CATTACCTTG TGCTAACCTCT CTTTTCTAG TCTTCATAAT TTCTTCAC	1460
	AATCTCTGAT TCTGTCAATG TCTTGAAATC AAGGCCAGC TGGAGGTGAA GAAGAGAATG	1520
30	TGACAGGCAC AGATGAATGG GAGTGAGGGA TAGTGGGTC AGGGCTGAGA GGAGAAGGAG	1580
	GGAGACATGA GCATGGCTGA GCCTGGACAA AGACAAAGGT GAGCAAAGGG CTCACGCATT	1640
	CAGCCAGGAG ATGATACTGG TCCTTAGCCC CATCTGCCAC GTGTATTTAA CCTTGAAGGG	1700
35	TTCACCAGGT CAGGGAGAGT TTGGGAAC TG CAATAACCTG GGAGTTTGG TGGAGTCCGA	1760
	TGATTCTCTT TTGCATAAGT GCATGACATA TTTTGCTTT ATTACAGTTT ATCTATGGCA	1820
40	CCCATGCACC TTACATTTGA AATCTATGAA ATATCATGCT CCATTGTTCA GATGCTTCTT	1880
	AGGCCACATC CCCCTGTCTA AAAATTCAAGA AAATTTTGT TTATAAAAGA TGCATTATCT	1940
	ATGATATGCT AATATATGTA TATGCAATAT AAAATTAG	1979

Leu Gly Leu Val Leu Pro Leu Leu Ile Met Val Ile Cys Tyr Ser Gly
 210 215 220

Ile Leu Lys Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg
 5 225 230 235 240

Ala Val Arg Val Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp
 245 250 255

10 Thr Pro Tyr Asn Ile Val Ile Leu Leu Asn Thr Phe Gln Glu Phe Phe
 260 265 270

Gly Leu Ser Asn Cys Glu Ser Thr Ser Gln Leu Asp Gln Ala Thr Gln
 275 280 285

15 Val Thr Glu Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile
 290 295 300

Tyr Ala Phe Val Gly Glu Lys Phe Arg Arg Tyr Leu Ser Val Phe Phe
 20 305 310 315 320

Arg Lys His Ile Thr Lys Arg Phe Cys Lys Gln Cys Pro Val Phe Tyr
 325 330 335

25 Arg Glu Thr Val Asp Gly Val Thr Ser Thr Asn Thr Pro Ser Thr Gly
 340 345 350

Glu Gln Glu Val Ser Ala Gly Leu
 355 360

30 (2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 355 amino acids
 35 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

40 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Glu Thr Pro Asn Thr Thr Glu Asp Tyr Asp Thr Thr Thr Glu Phe
 1 5 10 15

Asp Tyr Gly Asp Ala Thr Pro Cys Gln Lys Val Asn Glu Arg Ala Phe
 20 25 30

Gly Ala Gln Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Val Ile Gly
 5 35 40 45

Leu Val Gly Asn Ile Leu Val Val Leu Val Leu Val Gln Tyr Lys Arg
 50 55 60

10 Leu Lys Asn Met Thr Ser Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp
 65 70 75 80

Leu Leu Phe Leu Phe Thr Leu Pro Phe Trp Ile Asp Tyr Lys Leu Lys
 85 90 95

15 Asp Asp Trp Val Phe Gly Asp Ala Met Cys Lys Ile Leu Ser Gly Phe
 100 105 110

Tyr Tyr Thr Gly Leu Tyr Ser Glu Ile Phe Phe Ile Ile Leu Leu Thr
 20 115 120 125

Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Arg Ala
 130 135 140

25 Arg Thr Val Thr Phe Gly Val Ile Thr Ser Ile Ile Ile Trp Ala Leu
 145 150 155 160

Ala Ile Leu Ala Ser Met Pro Gly Leu Tyr Phe Ser Lys Thr Gln Trp
 165 170 175

30 Glu Phe Thr His His Thr Cys Ser Leu His Phe Pro His Glu Ser Leu
 180 185 190

Arg Glu Trp Lys Leu Phe Gln Ala Leu Lys Leu Asn Leu Phe Gly Leu
 35 195 200 205

Val Leu Pro Leu Leu Val Met Ile Ile Cys Tyr Thr Gly Ile Ile Lys
 210 215 220

40 Ile Leu Leu Arg Arg Pro Asn Glu Lys Lys Ser Lys Ala Val Arg Leu
 225 230 235 240

Ile Phe Val Ile Met Ile Ile Phe Phe Leu Phe Trp Thr Pro Tyr Asn
 245 250 255

45 Leu Thr Ile Leu Ile Ser Val Phe Gln Asp Phe Leu Phe Thr His Glu
 260 265 270

59.

Cys Glu Gln Ser Arg His Leu Asp Leu Ala Val Gln Val Thr Glu Val
 275 280 285

Ile Ala Tyr Thr His Cys Cys Val Asn Pro Val Ile Tyr Ala Phe Val
 5 290 295 300

Gly Glu Arg Phe Arg Lys Tyr Leu Arg Gln Leu Phe His Arg Arg Val
 305 310 315 320

10 Ala Val His Leu Val Lys Trp Leu Pro Phe Leu Ser Val Asp Arg Leu
 325 330 335

Glu Arg Val Ser Ser Thr Ser Pro Ser Thr Gly Glu His Glu Leu Ser
 340 345 350

15 Ala Gly Phe
 355

20 (2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 352 amino acids

(B) TYPE: amino acid

25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Glu Gly Ile Ser Ile Tyr Thr Ser Asp Asn Tyr Thr Glu Glu Met
 1 5 10 15

35 Gly Ser Gly Asp Tyr Asp Ser Met Lys Glu Pro Cys Phe Arg Glu Glu
 20 25 30

40 Asn Ala Asn Phe Asn Lys Ile Phe Leu Pro Tyr Ile Tyr Ser Ile Ile
 35 40 45

45 Phe Leu Tyr Gly Ile Val Gly Asn Gly Leu Val Ile Leu Val Met Gly
 50 55 60

Tyr Gln Lys Lys Leu Arg Ser Met Thr Asp Lys Tyr Arg Leu His Leu
 65 70 75 80

P 9 5 2 3 5 7 3 0 2 2 6 0 0

Ser Val Ala Asp Leu Leu Phe Val Ile Thr Leu Pro Phe Trp Ala Val
 85 90 95

Asp Ala Val Ala Asn Trp Tyr Phe Gly Asn Phe Leu Cys Lys Ala Val
 5 100 105 110

His Val Ile Tyr Thr Val Asn Leu Tyr Ser Ser Val Leu Ile Leu Ala
 115 120 125

10 Phe Ile Ser Leu Asp Arg Tyr Leu Ala Ile Val His Ala Thr Asn Ser
 130 135 140

Gln Arg Pro Arg Lys Leu Leu Ala Glu Lys Val Val Tyr Val Gly Val
 145 150 155 160

15 Trp Ile Pro Ala Leu Leu Leu Thr Ile Pro Asp Phe Ile Phe Ala Asn
 165 170 175

20 Val Ser Glu Ala Asp Asp Arg Tyr Ile Cys Asp Arg Phe Tyr Pro Asn
 180 185 190

Asp Leu Trp Val Val Val Phe Gln Phe Gln His Ile Met Val Gly Leu
 195 200 205

25 Ile Leu Pro Gly Ile Val Ile Leu Phe Cys Tyr Cys Ile Ile Ile Ser
 210 215 220

Lys Leu Ser His Ser Lys Gly His Gln Lys Arg Lys Ala Leu Lys Tyr
 225 230 235 240

30 Tyr Val Ile Leu Ile Leu Ala Phe Phe Ala Cys Trp Leu Pro Tyr Tyr
 245 250 255

Ile Gly Ile Ser Ile Asp Ser Phe Ile Leu Leu Glu Ile Ile Lys Gln
 35 260 265 270

Gly Cys Glu Phe Glu Asn Thr Val His Lys Trp Ile Ser Ile Thr Glu
 275 280 285

40 Ala Leu Ala Phe Phe His Cys Cys Leu Asn Pro Ile Leu Tyr Ala Phe
 290 295 300

Leu Gly Ala Lys Phe Lys Tyr Ser Ala Gln His Ala Leu Thr Ser Val
 305 310 315 320

45 Ser Arg Gly Ser Ser Leu Lys Ile Leu Ser Lys Gly Lys Arg Gly Gly
 325 330 335

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His Ser Ser Val Ser Thr Glu Ser Glu Ser Ser Ser Phe His Ser Ser
 340 345 350

5 (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 350 amino acids
 (B) TYPE: amino acid
 10 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

15 (iv) ANTI-SENSE: NO

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ser Asn Ile Thr Asp Pro Gln Met Trp Asp Phe Asp Asp Leu Asn
 1 5 10 15

25 Phe Thr Gly Met Pro Pro Ala Asp Glu Asp Tyr Ser Pro Cys Met Leu
 20 25 30

Glu Thr Glu Thr Leu Asn Lys Tyr Val Val Ile Ile Ala Tyr Ala Leu
 35 40 45

30 Val Phe Leu Leu Ser Leu Leu Gly Asn Ser Leu Val Met Leu Val Ile
 50 55 60

Leu Tyr Ser Arg Val Gly Arg Ser Val Thr Asp Val Tyr Leu Leu Asn
 65 70 75 80

Leu Ala Leu Ala Asp Leu Leu Phe Ala Leu Thr Leu Pro Ile Trp Ala
 85 90 95

40 Ala Ser Lys Val Asn Gly Trp Ile Phe Gly Thr Phe Leu Cys Lys Val
 100 105 110

Val Ser Leu Leu Lys Glu Val Asn Phe Tyr Ser Gly Ile Leu Leu Leu
 115 120 125

45 Ala Cys Ile Ser Val Asp Arg Tyr Leu Ala Ile Val His Ala Thr Arg
 130 135 140

DRAFT DRAFT DRAFT DRAFT DRAFT

Thr Leu Thr Gln Lys Arg His Leu Val Lys Phe Val Cys Leu Gly Cys
 145 150 155 160

Trp Gly Leu Ser Met Asn Leu Ser Leu Pro Phe Phe Leu Phe Arg Gln
 5 165 170 175

Ala Tyr His Pro Asn Asn Ser Ser Pro Val Cys Tyr Glu Val Leu Gly
 180 185 190

10 Asn Asp Thr Ala Lys Trp Arg Met Val Leu Arg Ile Leu Pro His Thr
 195 200 205

Phe Gly Phe Ile Val Pro Leu Phe Val Met Leu Phe Cys Tyr Gly Phe
 210 215 220

15 Thr Leu Arg Thr Leu Phe Lys Ala His Met Gly Gln Lys His Arg Ala
 225 230 235 240

Met Arg Val Ile Phe Ala Val Val Leu Ile Phe Leu Leu Cys Trp Leu
 20 245 250 255

Pro Tyr Asn Leu Val Leu Leu Ala Asp Thr Leu Met Arg Thr Gln Val
 260 265 270

25 Ile Gln Glu Thr Cys Glu Arg Arg Asn Asn Ile Gly Arg Ala Leu Asp
 275 280 285

Ala Thr Glu Ile Leu Gly Phe Leu His Ser Cys Leu Asn Pro Ile Ile
 290 295 300

30 Tyr Ala Phe Ile Gly Gln Asn Phe Arg His Gly Phe Leu Lys Ile Leu
 305 310 315 320

Ala Met His Gly Leu Val Ser Lys Glu Phe Leu Ala Arg His Arg Val
 35 325 330 335

Thr Ser Tyr Thr Ser Ser Val Asn Val Ser Ser Asn Leu
 340 345 350

40 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 355 amino acids
 (B) TYPE: amino acid
 45 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

5	Met Glu Ser Asp Ser Phe Glu Asp Phe Trp Lys Gly Glu Asp Leu Ser	1	5	10	15
	Asn Tyr Ser Tyr Ser Ser Thr Leu Pro Pro Phe Leu Leu Asp Ala Ala	20		25	30
10	Pro Cys Glu Pro Glu Ser Leu Glu Ile Asn Lys Tyr Phe Val Val Ile	35	40	45	
	Ile Tyr Ala Leu Val Phe Leu Leu Ser Leu Leu Gly Asn Ser Leu Val	50	55	60	
15	Met Leu Val Ile Leu Tyr Ser Arg Val Gly Arg Ser Val Thr Asp Val	65	70	75	80
20	Tyr Leu Leu Asn Leu Ala Leu Ala Asp Leu Leu Phe Ala Leu Thr Leu	85	90	95	
	Pro Ile Trp Ala Ala Ser Lys Val Asn Gly Trp Ile Phe Gly Thr Phe	100	105	110	
25	Leu Cys Lys Val Val Ser Leu Leu Lys Glu Val Asn Phe Tyr Ser Gly	115	120	125	
	Ile Leu Leu Ala Cys Ile Ser Val Asp Arg Tyr Leu Ala Ile Val	130	135	140	
30	His Ala Thr Arg Thr Leu Thr Gln Lys Arg Tyr Leu Val Lys Phe Ile	145	150	155	160
	Cys Leu Ser Ile Trp Gly Leu Ser Leu Leu Leu Ala Leu Pro Val Leu	165	170	175	
35	Leu Phe Arg Arg Thr Val Tyr Ser Ser Asn Val Ser Pro Ala Cys Tyr	180	185	190	
40	Glu Asp Met Gly Asn Asn Thr Ala Asn Trp Arg Met Leu Leu Arg Ile	195	200	205	
	Leu Pro Gln Ser Phe Gly Phe Ile Val Pro Leu Leu Ile Met Leu Phe	210	215	220	
45	Cys Tyr Gly Phe Thr Leu Arg Thr Leu Phe Lys Ala His Met Gly Gln	225	230	235	240

Lys His Arg Ala Met Arg Val Ile Phe Ala Val Val Leu Ile Phe Leu
 245 250 255

5 Leu Cys Trp Leu Pro Tyr Asn Leu Val Leu Leu Ala Asp Thr Leu Met
 260 265 270

Arg Thr Gln Val Ile Gln Glu Thr Cys Glu Arg Arg Asn His Ile Asp
 275 280 285

10 Arg Ala Leu Asp Ala Thr Glu Ile Leu Gly Ile Leu His Ser Cys Leu
 290 295 300

Asn Pro Leu Ile Tyr Ala Phe Ile Gly Gln Lys Phe Arg His Gly Leu
 305 310 315 320

15 Leu Lys Ile Leu Ala Ile His Gly Leu Ile Ser Lys Asp Ser Leu Pro
 325 330 335

20 Lys Asp Ser Arg Pro Ser Phe Val Gly Ser Ser Ser Gly His Thr Ser
 340 345 350

Thr Thr Leu
 355

25 (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

35 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
 CGCTCGAGAC CTRKCMDTKK CYGACCT

45 (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid

- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

10 Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val
1 5 10 15

His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe Gly Val
20 25 30

15 (2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

25

Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val
1 5 10 15

30 His Ala Val Phe Ala Leu Arg Ala Arg Thr Val Thr Phe Gly Val
20 25 30